IN THE CLAIMS:

1-26. (cancelled)

27. (previously presented) A method of identifying a pathogen in a sample comprising the steps of:

amplifying a plurality of segments of nucleic acid of said pathogen with a plurality of primer pairs to obtain a plurality of amplification products; and

determining base compositions of at least two members of said plurality of amplification products wherein said base compositions are calculated from molecular mass measurements of the amplification products using a mass spectrometer, wherein the base compositions identify the number of each individual nucleotide present in said amplification products without sequencing said amplification product, and wherein the base compositions identify said pathogen in said sample.

28. (previously presented) The method of claim 27 wherein the pathogen is a bacterium, a virus, a protozoan, a parasite, a mold, or a fungus.

29. (previously presented) The method of claim 27 wherein said sample is a biological sample comprising blood, mucus, hair, urine, breath, sputum, saliva, stool, nail, or tissue.

30. (cancelled)

31. (previously presented) The method of claim 27 wherein said sample is obtained from a human.

32. (previously presented) The method of claim 27 wherein said plurality of primer pairs comprises broad range survey primer pairs, division-wide primer pairs, drill-down primer pairs, or any combination thereof.

33. (previously presented) The method of claim 27 wherein identification of said pathogen is accomplished at the genus or species level, and wherein said plurality of primer pairs comprises broad range survey primer pairs or division-wide primer pairs.

34. (previously presented) The method of claim 32 further comprising identifying a subspecies characteristic of said pathogen from the base compositions of at least two drill-down amplification products obtained using a plurality of drill-down primer pairs.

35. (previously presented) The method of claim 34 wherein said subspecies characteristic is a serotype, a strain type, a sub-strain type, a sub-species type, an emm-type, a bioengineered gene, a toxin gene, an antibiotic resistance gene, a pathogenicity island, or a virulence factor.

36. (cancelled)

37. (previously presented) The method of claim 27 wherein said mass spectrometry is Fourier transform ion cyclotron resonance mass spectrometry (FTICR- MS), ion trap mass spectrometry, quadrupole mass spectrometry, magnetic sector mass spectrometry, time of flight (TOF) mass spectrometry, Q-TOF mass spectrometry, or triple quadrupole mass spectrometry.

38. (previously presented) The method of claim 27 wherein each member of each primer pair of said plurality of primer pairs hybridizes to nucleic acid encoding ribosomal RNA or a housekeeping gene.

39-49. (cancelled)

50. (previously presented) The method of claim 38 wherein said housekeeping gene encodes a protein that participates in translation, replication, recombination, repair,

transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, uptake, secretion, antibiotic resistance, virulence, or pathogenicity.

51. (previously presented) The method of claim 38 wherein said housekeeping gene is a polymerase.

52. (previously presented) The method of claim 27 wherein said pathogen is a previously unknown pathogen.

53. (previously presented) A method for characterizing a strain type of a pathogen comprising:

amplifying nucleic acid of said pathogen with a plurality of primer pairs that hybridize to a plurality of segments of nucleic acid of said pathogen to obtain a plurality of amplification products, wherein one or more base compositions of said plurality of amplification products differs among different strain types of said pathogen; and

determining base compositions of each member of said plurality of amplification products to obtain a series of base compositions, wherein said base compositions are calculated from molecular mass measurements of the amplification products using a mass spectrometer, wherein the base compositions identify the number of each individual nucleotide present in said amplification products without sequencing said amplification product, thereby characterizing said strain type.

54. (previously presented) The method of claim 53 wherein said pathogen is a bacterium, a virus, a protozoan, a parasite, a mold or a fungus.

55. (previously presented) The method of claim 53 wherein said pathogen is obtained from a biological sample.

56. (previously presented) The method of claim 55 wherein said biological sample comprises blood, mucus, hair, urine, breath, sputum, saliva, stool, nail, or tissue.

57. (previously presented) The method of claim 55 wherein said biological sample is obtained from a human.

58. (previously presented) The method of claim 53 wherein said plurality of primer pairs comprises broad range survey primers primer pairs, division-wide primers primer pairs, or drill-down primers primer pairs, or any combination thereof.

59. (previously presented) The method of claim 53 wherein said pathogen comprises a sub-species characteristic.

60. (previously presented) The method of claim 59 wherein said sub-species characteristic is a serotype, a strain type, a sub-strain type, a sub-species type, an emm-type, a bioengineered gene, a toxin gene, an antibiotic resistance gene, a pathogenicity island, or a virulence factor.

61. (cancelled)

62. (previously presented) The method of claim 53 wherein said mass spectrometry is Fourier transform ion cyclotron resonance mass spectrometry (FTICR- MS), ion trap mass spectrometry, quadrupole mass spectrometry, magnetic sector mass spectrometry, time of flight (TOF) mass spectrometry, Q-TOF mass spectrometry, or triple quadrupole mass spectrometry.

63. (previously presented) The method of claim 53 wherein members of said plurality of primer pairs hybridize to nucleic acid encoding ribosomal RNA or housekeeping genes.

64. (previously presented) The method of claim 63 wherein said housekeeping genes encode proteins that participate in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, uptake, secretion, antibiotic resistance, virulence, or pathogenicity.

65. (previously presented) The method of claim 63 wherein one or more of said housekeeping genes encodes a polymerase.

66. (previously presented) The method of claim 53 wherein said plurality of primer pairs comprises four or more primer pairs.

67. (previously presented) The method of claim 53 wherein said strain type is a previously unknown strain type.

68. (previously presented) The method of claim 53 further comprising associating said plurality of base compositions with a known strain of said pathogen, thereby identifying the strain type of said pathogen.

69. (previously presented) A method of screening a biological sample to determine the presence or absence of a pathogen comprising:

contacting nucleic acid of said sample with one or more primer pairs under amplification conditions wherein

production of one or more amplification products whose base compositions match known base compositions of amplification products of nucleic acid of said pathogen produced with said one or more primer pairs indicates the presence of said pathogen, wherein said base compositions are calculated from molecular mass measurements of the one or more amplification products using a mass spectrometer, wherein the base compositions identify the number of each individual nucleotide present in said one or more amplification products without sequencing said amplification product; or

wherein failure to produce one or more amplification products whose base compositions match said known base compositions indicates the absence of said pathogen.

70. (previously presented) The method of claim 69 wherein said pathogen is a bacterium virus, protozoan, parasite, mold, or fungus.

71. (previously presented) The method of claim 69 wherein said biological sample comprises blood or tissue.

72. (cancelled)

73. (previously presented) The method of claim 69 wherein said mass spectrometry is Fourier transform ion cyclotron resonance (FTICR) mass spectrometry, ion trap mass spectrometry, quadrupole mass spectrometry, magnetic sector mass spectrometry, time-of-flight (TOF) mass spectrometry, Q-TOF mass spectrometry or triple quadrupole mass spectrometry.

74. (previously presented) The method of claim 69 wherein said one or more primer pairs hybridize to nucleic acid encoding ribosomal RNA or housekeeping genes.

75. (previously presented) A method of identifying one or more etiologic agents of disease in a sample comprising the steps of:

amplifying a segment of nucleic acid from said one or more of etiologic agents in said sample with one or more primer pairs to obtain one or more amplification products;

determining base compositions of said one or more amplification products, wherein said base compositions are calculated from molecular mass measurements of the amplification products using a mass spectrometer, wherein the base compositions identify the number of each individual nucleotide present in said amplification products without sequencing said amplification product; and

comparing said base compositions with known base compositions of known etiologic agents produced with said one or more primer pairs, thereby identifying said one or more etiologic agents in said sample.

76. (previously presented) The method of claim 75 wherein identification of said one or more etiologic agents is accomplished at the genus or species level, and said one or more primer pairs comprise broad range survey primer pairs, division-wide primer pairs or any combination thereof.

77. (previously presented) The method of claim 75 further comprising identifying a subspecies characteristic of said one or more etiologic agents from the base composition of a drill-down amplification product produced with a drill-down primer pair.

78. (previously presented) The method of claim 77 wherein said subspecies characteristic is a serotype, a strain type, a sub-strain type, a sub-species type, an emm-type, a bioengineered gene, a toxin gene, an antibiotic resistance gene, a pathogenicity island, or a virulence factor.

79. (cancelled)

80. (previously presented) The method of claim 75 wherein said mass spectrometry is Fourier transform ion cyclotron resonance mass spectrometry (FTICR- MS), ion trap mass spectrometry, quadrupole mass spectrometry, magnetic sector mass spectrometry, time of flight (TOF) mass spectrometry, Q-TOF mass spectrometry, or triple quadrupole mass spectrometry.

81. (previously presented) The method of claim 75 wherein said one or more etiologic agents comprise a bacterium, a virus, a protozoan, a parasite, a mold, a fungus, or any combination thereof.

82. (previously presented) The method of claim 75 wherein said sample is a biological sample comprising blood, mucus, hair, urine, breath, sputum, saliva, stool, nail, or tissue.

83. (previously presented) The method of claim 75 wherein said sample is obtained from a human.

84. (previously presented) The method of claim 75 wherein said one or more primer pairs hybridize to nucleic acid encoding ribosomal RNA or housekeeping genes.

85. (previously presented) The method of claim 84 wherein said housekeeping genes encode proteins that participate in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, uptake, secretion, antibiotic resistance, virulence, or pathogenicity.

86. (previously presented) The method of claim 84 wherein one or more of said housekeeping genes encode a polymerase.

87. (previously presented) The method of claim 75 wherein said one or more etiologic agents are previously unknown etiologic agents.